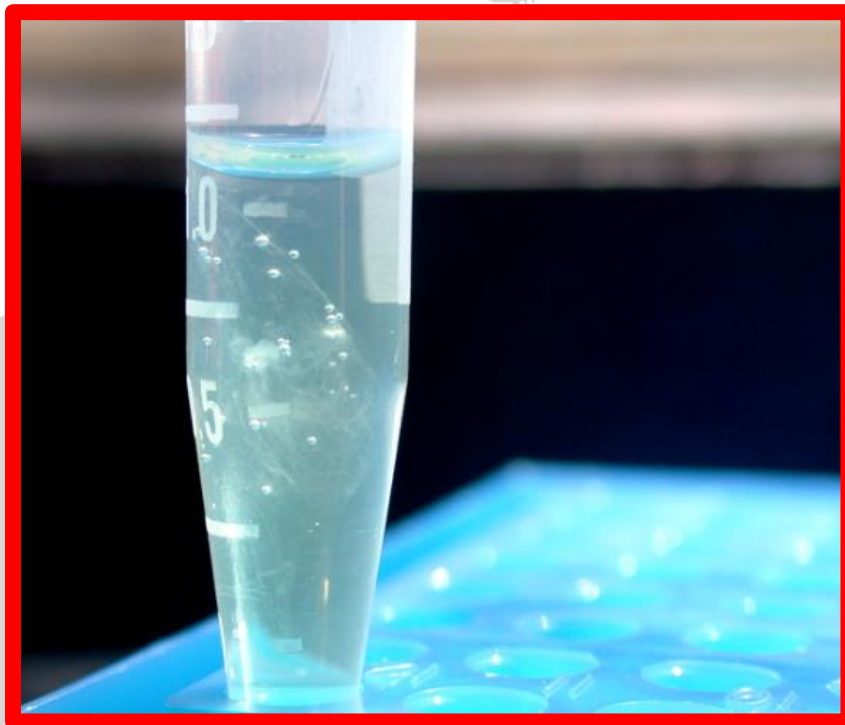


FishGen

User Manual v1.0

January 20th, 2014



FishGen (<http://www.fishgen.net/>) is a final repository for salmon and steelhead genetic data as part of Genetic Stock Identification and Parentage Based Tagging projects in the Columbia River basin and throughout the Pacific Coast of North America. FishGen was developed by Resource Data, Inc. (RDI) for the Idaho Department of Fish and Game with funding from the Pacific Coast Salmon Recovery Fund.

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Questions/Help

Please contact Jesse McCane or Matt Campbell if you have any questions about FishGen or need any assistance:

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Home Page

You can browse the database and learn about collaborating labs without logging in. To learn about fish genetics labs that contribute to conservation and management of steelhead and salmon, click [Learn about collaborating labs](#). If you are interested in uploading or downloading data you need to be a registered user and *Log In* with your username and password. If you are not registered, click [Register](#) in the upper right corner of the screen.

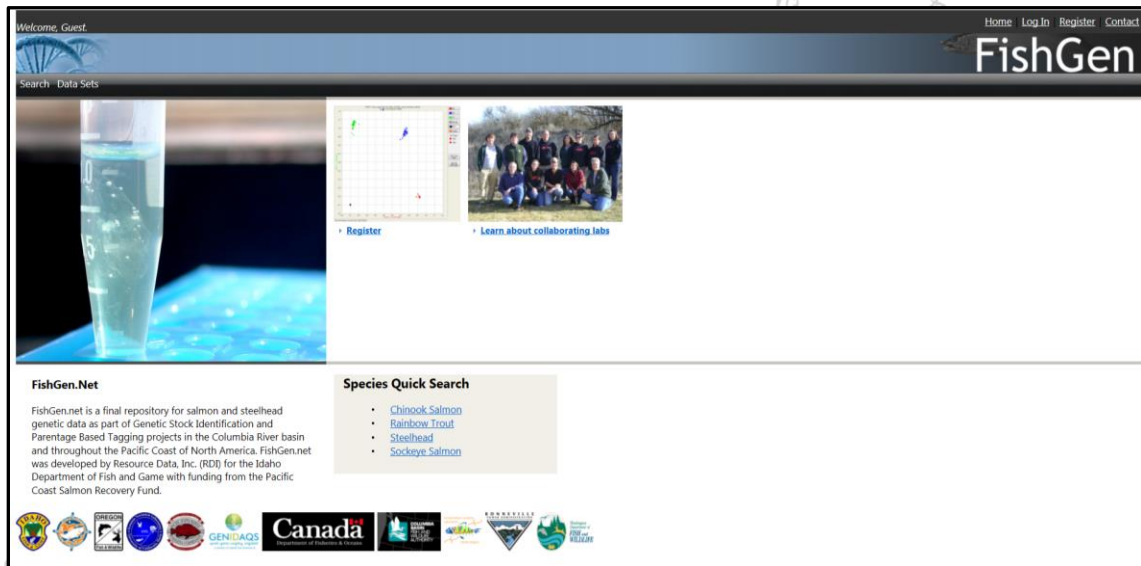


Figure 1. Home Page. In this example the user is a guest.

From this page, you may login or register for an account. To complete registration, click the [Register](#) heading.

Request Account Page

The **Request Account** page opens.

Required fields are denoted with an asterisk (*). After filling in the form with all required information, click the *Send Request* button. An e-mail will be sent to the FishGen curator who will verify the data and set up the login. A return e-mail will be sent from the curator notifying you that the login is ready to use. This will usually just take a few minutes.

Welcome, Guest

Home Log In Register Contact

FishGen

Search Data Sets

Request Account

* denotes a required field

*Email Address:	<input type="text"/>	*Organization:	<input type="text"/>
*Password:	<input type="text"/>	Other Organization:	<input type="text"/>
*Re-enter Password:	<input type="text"/>	Street Address 1:	<input type="text"/>
Password Hint:	<input type="text"/>	Street Address 2:	<input type="text"/>
*First Name:	<input type="text"/>	City:	<input type="text"/>
*Last Name:	<input type="text"/>	State:	<input type="text"/>
Phone:	<input type="text"/>	Zip Code:	<input type="text"/>

Send Request

Figure 2. Request Account page.

Uploading genetic markers

Before genetic data can be successfully uploaded on FishGen, the genetic markers in your dataset must be defined and uploaded in the database. The three marker types FishGen currently accepts are microsatellites, Taqman SNPs (SNP), and RAD SNPs (RAD). To define markers in FishGen only requires that a small text file be uploaded that provides the name and the necessary DNA sequence, primer/probe sequence, marker name and allelic information. This information is necessary to ensure that genetic markers used in FishGen are standardized and not duplicated.

Uploading Microsatellite markers-

Microsatellite markers are not species specific in FishGen. The only information necessary to upload microsatellite markers in the database is the marker name and the forward and reverse primer sequences. This information can be saved in tab delimited text file as shown below. Marker names must be unique and during the upload, FishGen will check to make sure the marker name has not already been used. FishGen will also check to ensure that the primer sequences provided have not already been assigned to a previous marker name in the database. Most labs using this database will be familiar with the GAPS (Chinook salmon) and SPAN (steelhead) microsatellite marker sets that have been standardized among PNW fish genetic labs. These microsatellite markers have already been uploaded into FishGen.

Marker Name	Forward Primer	Reverse Primer
Ots1	GGAAAGAGCAGATGTTGTTAA	TGCTTTATCTGCTGCTTCA
Ogo1a	GATCTGGGCTTAAGGGAAC	ACTAGCGTTGGAGAACCC
Ogo4	GTCGTCAGTGGCATCAGCTA	GAGTGGAGATGCAGCCAAAG
Omy325	TGTGAGACTGTCAGATTTTGC	CGAGTCCGTATCCTTCCC
Oneu10.2	TGTGGACCACTTGTAAACAG	CTGTAGGTGTGAAATGTATTTAA
Ots3M	TGTCACTCACACTCTTTCAAGGAG	GAGAGTGCTGTCCAAAGGTGA
Omm1080	GAGACTGACACGGGTATTGA	GTTATGTTGTATGCCTAGGG
Omy1011	AACTTGTCTATGTGAATGTGC	GACAAAGTGACTGGTTGGT
Ots211	TAGGTTACTGCTTCGTCATATG	GAGAGGTGGTAGGATTTGAG
Ots9	ATCAGGGAAAGCTTTGGAGA	CCTCTGTTTACAGCTAGCA
Ots213	CCTACTCATGTCTCTATTTGGTG	AGCCAAGGCATTTCTAAGTGAC
Oki23	TGTGCTATAGGGTGAATGTGC	AACACAGGCATCCCCACTAA
Ots208b	GGATGAAGTGCAGCTTGTATG	GGCAATCACATACTCAACTTCC
Ots212	TCTTTCCCTGTTCTCGCTTC	CCGATGAAGAGCAGAAGAGAC
OtsG474	TTAGCTTTGGACATTTTATCACAC	CCAGAGCAGGGACCAGAAC
Ogo2	ACATCGCACACCATAAGCAT	GTTCCTTCGACTGTTCTCTGTGTTGAG
Oki100	CCAGCACTCTCACTATTT	CCAGAGTAGTCATCTCTG
Ssa408	AATGGATTACGGGTACGTTAGACA	CTCTTGTGCAAGTTCTTCATCTGT
Ots201b	CAGGCGTGACAATTATGC	TGGACATCTGTGCGTTGC
OtsG249	TTCTCAGAGGGTAAAATCTCAGTAAG	GTACAACCCCTCTCACCTACCC
OtsG68	TATGAACGTCAGCTTGTATGTTAGT	CATGTGCGCTGCTCAATGTA
OtsG432	TGAAAAGTAGGGGAAACACATACG	TAAAGCCCATTTGAATTGAATAGAA
Sfo8	CAACGAGCACAGAACAGG	CTTCCCTGGAGAGGAAA
Oneu11	GTTCGGATGACTCAGATGGGACT	TCATCTTTTCTGTCAACTTCCA
Ots4	GACCCAGAGCACAGCACAA	GGAGGACACATTTCAAGCAG
Oneu8	AACATTCTGGGATGACAGGGGTA	CTGTTCTGCTCCAGTGAAGTGA
Oneu14	AGAAACATGAGAAGCTAGGT	CCTTATGAGTTTGGTCTCCATGT
Ots100	TGAACATGAGCTGTGTGAG	ACGGACGTGCCAGTGAG
Omy27	TTTATGTCATGTCAGCCAGTG	TTTATGGCTGGCAACTAATGT
Omy7	TTAAGTTTTGCCTAGATAAGGG	CAAGGAATGGCACAGCTTG
Ots3	CACACTCTTTCAAGGAG	CTTCATTGTGATTCT
Ssa289	CTTTACAAATAGACAGACT	TCATACAGTCACTATCATC
Ssa407	TGTGTAGGCAGGTGTGGAC	CACTGCTGTTACTTTGGTGATTC
Oke4	AGGCCAAAGTCTGTAGTGAAGG	GATGAATCGAGAGAATAGGGACTGAAT
Omy1001	GATTCCATAACCTCGCCTTC	GTCCTTGTGCTGCCTGCT

Figure 3. Example of a tab delimited text file needed to upload microsatellite marker information.

To upload the marker definition file, select the Upload Marker tab under Contributor.

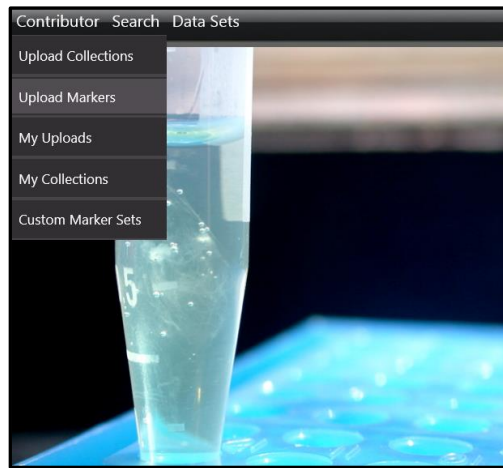


Figure 4. Selecting “Upload Marker” under Contributor tab.

This will bring you to the upload marker page where you can browse to find your text file.

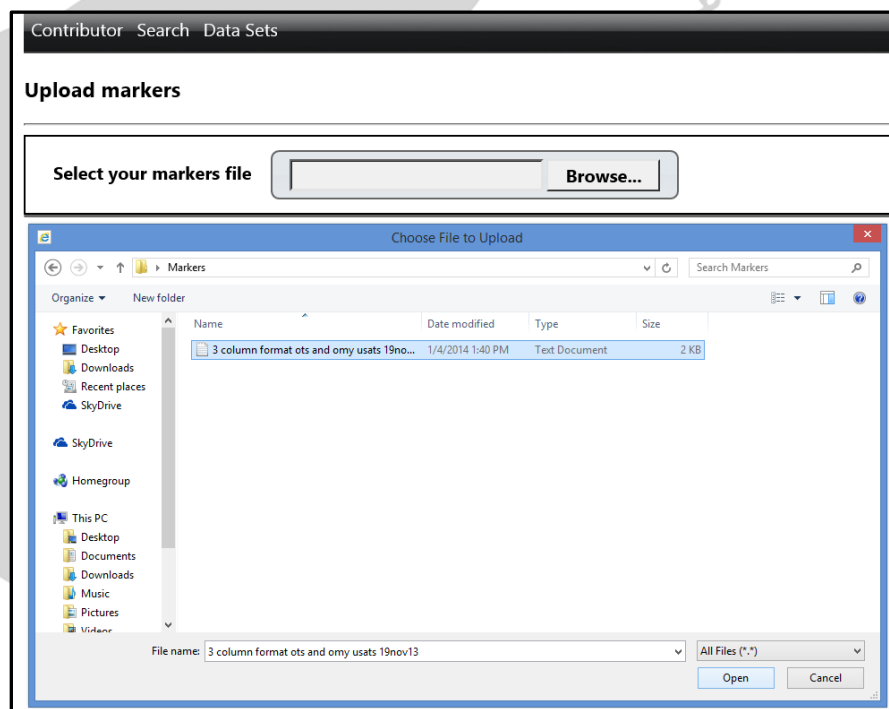


Figure 5. Selecting markers file.

After the text file has opened, you will need to provide the following information:

Data Formatting-

- Check the box if the first row in your marker definition file is a header row.
- Select the delimiter (tab, comma, or space)

Marker Type-

- Select Microsatellite

The 'Upload markers' dialog box is shown with the 'Marker Configuration' section active. The 'Marker Type' dropdown menu is open, showing 'Microsatellite' as the selected option. Other options visible are 'RAD' and 'SNP'. The 'Data Formatting' section has 'First row is Header' checked and 'Tab' selected as the delimiter. The 'Additional Upload Options' section has 'Save Column Mapping' and 'Save Marker Set' unchecked, and 'Use Saved Column Mapping' set to '[Select Mapping]'. Below these sections is a table with three columns: 1, 2, and 3. Each column has a dropdown menu set to '<Ignore Field>'. The table contains the following data:

Marker_Name	Forward Primer	Reverse Primer
Ots1	GGAAAGAGCAGATGTTGTAA	TGCTTTATCTGCTGCTTCA
Ogo1a	GATCTGGGCCTAAGGAAAC	ACTAGCGGTTGGAGAACCC
Ogo4	GTCGTCACTGGCATCAGCTA	GAGTGGAGATCGAGCCAAAG

Figure 6. Selecting marker type during marker upload.

Additional Upload Options-

If you would like to save the markers that you are uploading as a unique marker set, one that you can select during data exporting, check the box labeled “Save Marker Set” and provide a name.

Selecting Fields-

Finally, select which columns contain the Marker Name, the Forward Primer and the Reverse Primer.

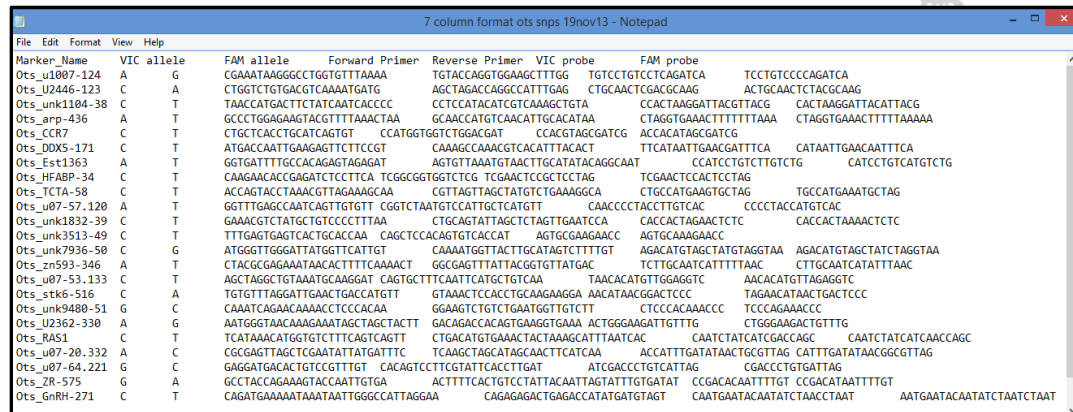
The 'Upload markers' dialog box is shown with the 'Selecting Fields' section active. The 'Marker Configuration' section has 'Marker Type' set to 'Microsatellite' and 'Select Species' set to 'Acipenser transmontanus'. The 'Additional Upload Options' section has 'Save Column Mapping' and 'Save Marker Set' unchecked, and 'Use Saved Column Mapping' set to '[Select Mapping]'. Below these sections is a table with three columns: 1, 2, and 3. Each column has a dropdown menu. The table contains the following data:

Marker_Name	Forward Primer	Reverse Primer
Ots1	GGAAAGAGCAGATGTTGTAA	TGCTTTATCTGCTGCTTCA
Ogo1a	GATCTGGGCCTAAGGAAAC	ACTAGCGGTTGGAGAACCC
Ogo4	GTCGTCACTGGCATCAGCTA	GAGTGGAGATCGAGCCAAAG

Figure 7. Selecting column headers during marker upload.

Uploading SNP markers-

The term “SNP” in this database describes a marker that interrogates a SNP using a forward and reverse primer and two allele-specific probes (i.e. Taqman SNP assays). The procedures for uploading SNP marker names and definitions are similar as those used for Microsatellite markers. However, SNPs are species specific in FishGen, and the user must provide VIC and FAM probe sequences and VIC and FAM allele designations, along with forward and reverse primers in the marker definition text file. FishGen will check Marker Names, Primer and Probes sequences and allele designations to ensure Marker standardization. This prevents different SNPs from being uploaded into FishGen under the same name and prevents the same SNP being uploaded under different marker names.



Marker_Name	VIC allele	FAM allele	Forward Primer	Reverse Primer	VIC probe	FAM probe
Ots_u1087-124	A	G	CGAAATAGGGCTGGTGTAAAA	TGTACCAAGTGGAGCTTTGG	TGTCTGTCTCAGATCA	TCCTGTCCCCAGATCA
Ots_u2446-123	C	A	CTGGCTGTGACGTCAAAATGATG	AGCTAGACCAAGCCATTGG	CTGCAACTCGACGCAAG	ACTGCAACTCTACGCAAG
Ots_unk1104-38	C	T	TAACCATGACTTCTATCAATCACCCC	CCTCCATACATGCTCAAAAGCTGA	CCACTAAGGATTACGTTACG	CACTAAGGATTACATTACG
Ots_arp-436	A	T	GCCTCGGAGAGTACGTTTTAACTAA	GCACCATGTCAACATTGCACATAA	CTAGGTGAACCTTTTTTAA	CTAGGTGAACCTTTTTTAA
Ots_CCR7	C	T	CTGCTCCTGCATCAGTG	CCATGGTGTCTGGACGAT	CCACGTAGCGATCG	ACCACATAGCGATCG
Ots_DMX5-171	C	T	ATGACCAATTGAAGAGTCTTCCTCG	CAAAGCAAACTGCACATTACACT	TTCAATAATTGAACGATTTC	CATAATTGAACCAATTTC
Ots_Est1363	A	T	GGTGATTTTGCACAGAGTAGAGAT	AGTGTAAATGTAAGTGCATATACAGGCAAT	CCATCTGTCTGTCTG	CATCTGTCTGTCTG
Ots_HFABP-34	C	T	CAAGAACCAGAGATCTCTTCA	TCGGGGTGTCTCG	TCGAACCTCGCTCTAG	TCGCACTCACTCTAG
Ots_TCTA-58	C	T	ACCATCTAAAGCTTAGAAGCAA	CGTAGTTAGCTATGCTGAAGGCA	CTGCCATGAAGTGTCTAG	TGCCATGAAGTGTCTAG
Ots_u07-57.120	A	T	GGTTTGAGCAATCAGTTGTGTT	CGGTCTAATGTCATTGCTCATGTT	CAACCCCTACCTGTCTAC	CCCTTACATGTCTAC
Ots_unk1832-39	C	T	GAACGCTATGCTGTCCCTTTAA	CTGCAGTATTAGCTAGTTGAATCCA	CACCACTAGAATCTCTC	CACCACTAGAATCTCTC
Ots_unk3513-49	C	T	TTTGAGTGAGTCACTGCACCAA	CAGCTCCACAGTGTCCACAT	AGTGCAGGAAGCC	AGTGCAGGAAGCC
Ots_unk7936-50	C	G	ATGGGTGGGATTATGTTCTATTG	CAAAATGGTTACTTGCATAGCTTTTGT	AGACATGTAGCTATGTAGTAA	AGACATGTAGCTATGTAGTAA
Ots_zn593-346	A	T	CTACGCGAGAAATAACACTTTTCAAACT	GGCGAGTTTATTACGGTGTATGAC	TCTTGCAATCAATTTTAA	CTTGCAATCAATTTTAA
Ots_u07-53.133	C	T	AGCTAGGCTGTAAATGCAAGGAT	CAGTGCTTCAATTCTGCTCAA	TAACACATGTTGGAGTC	AACACATGTTAGAGGTC
Ots_s146-516	C	A	TGTGTTTAGGATTGAATGACATGTT	CTAAACTCACTGCAAGGAAGGA	AACTAAGCGACTCC	TAGAACAATGACTGCTCC
Ots_unk9488-51	G	C	CAATCAGAACAAACCTCCACAA	GGAGCTGTCTGAATGGTGTCTT	CTCCCAACAACCC	TCGCCAACAACCC
Ots_U2362-330	A	G	AATGGGTAAACAAAGATAGCTAGTACTT	GACAGACCACAGTGAAGTGAAA	ACTGGGAAGATTGTTT	CTGGGAAGACTGTTT
Ots_RAS1	C	T	TCATAAATAGTGTCTTTTCACTAGTT	CTGACATGTGAATCACTAAGCTTTAATCAC	CAATCTATCATCGACGAGC	CAATCTATCATCGACGAGC
Ots_u07-20.332	A	C	CGGAGTGTAGCTGAATATTATGATTTC	TCAGCTAGCATAGCAACTTCATCAA	ACCATTGATATAACTGCGTTAG	CATTGATATAAGCGCGTTAG
Ots_u07-64.221	G	C	GAGGATGACACTGCTGTTTGT	CACAGTCTCTGATTACCTTGTAT	ATGCACCTGTCTATTAG	CGACCTGTGATTAG
Ots_ZR-575	G	A	GCCTACAGAAATACCAATTGTGA	ACTTTTCACTGTCTATTACAATTAGTATTTGATAT	CCGACACAATTTTGT	CCGACACAATTTTGT
Ots_GnRH-271	C	T	CAGATGAAAATAAATTTGGCCATTAGAA	CAGAGAGACTGAGACATATGATGTAGT	CAATGAATACATATCTAACCTAAT	AATGAATACATATCTAACCTAAT

Figure 8. Tab delimited text file needed to upload SNP marker information.

After the text file has opened, you will need to provide the following information:

Data Formatting-

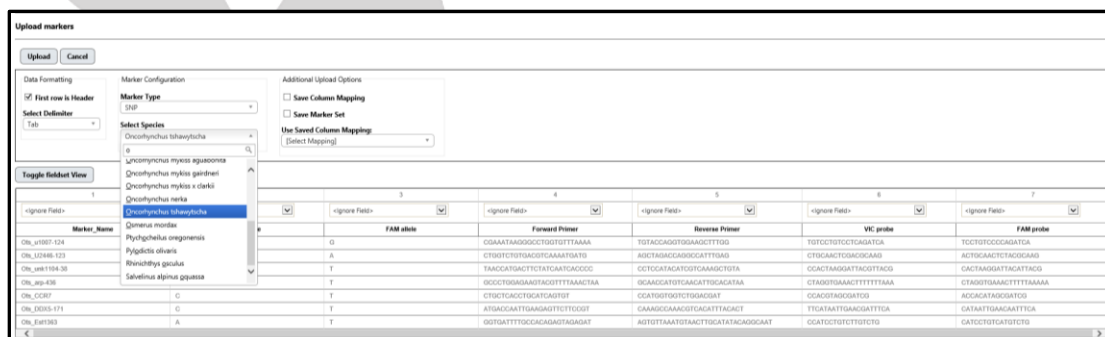
- Check the box if the first row in your marker definition file is a header row.
- Select the delimiter (tab, comma, or space)

Marker Type-

- Select SNP

Select Species-

- Select species that the SNP marker is screened on.



Upload markers

Data Formatting

☒ First row is Header

Select Delimiter: Tab

Marker Configuration

Marker Type: SNP

Select Species: Oryzias latipes

Additional Upload Options

☐ Save Column Mapping

☐ Save Marker Set

Use Saved Column Mapping: [Select Mapping]

Marker Name	VIC allele	FAM allele	Forward Primer	Reverse Primer	VIC probe	FAM probe
Ots_u1087-124	A	G	CGAAATAGGGCTGGTGTAAAA	TGTACCAAGTGGAGCTTTGG	TGTCTGTCTCAGATCA	TCCTGTCCCCAGATCA
Ots_u2446-123	C	A	CTGGCTGTGACGTCAAAATGATG	AGCTAGACCAAGCCATTGG	CTGCAACTCGACGCAAG	ACTGCAACTCTACGCAAG
Ots_unk1104-38	C	T	TAACCATGACTTCTATCAATCACCCC	CCTCCATACATGCTCAAAAGCTGA	CCACTAAGGATTACGTTACG	CACTAAGGATTACATTACG
Ots_arp-436	A	T	GCCTCGGAGAGTACGTTTTAACTAA	GCACCATGTCAACATTGCACATAA	CTAGGTGAACCTTTTTTAA	CTAGGTGAACCTTTTTTAA
Ots_CCR7	C	T	CTGCTCCTGCATCAGTG	CCATGGTGTCTGGACGAT	CCACGTAGCGATCG	ACCACATAGCGATCG
Ots_DMX5-171	C	T	ATGACCAATTGAAGAGTCTTCCTCG	CAAAGCAAACTGCACATTACACT	TTCAATAATTGAACGATTTC	CATAATTGAACCAATTTC
Ots_Est1363	A	T	GGTGATTTTGCACAGAGTAGAGAT	AGTGTAAATGTAAGTGCATATACAGGCAAT	CCATCTGTCTGTCTG	CATCTGTCTGTCTG
Ots_HFABP-34	C	T	CAAGAACCAGAGATCTCTTCA	TCGGGGTGTCTCG	TCGAACCTCGCTCTAG	TCGCACTCACTCTAG
Ots_TCTA-58	C	T	ACCATCTAAAGCTTAGAAGCAA	CGTAGTTAGCTATGCTGAAGGCA	CTGCCATGAAGTGTCTAG	TGCCATGAAGTGTCTAG
Ots_u07-57.120	A	T	GGTTTGAGCAATCAGTTGTGTT	CGGTCTAATGTCATTGCTCATGTT	CAACCCCTACCTGTCTAC	CCCTTACATGTCTAC
Ots_unk1832-39	C	T	GAACGCTATGCTGTCCCTTTAA	CTGCAGTATTAGCTAGTTGAATCCA	CACCACTAGAATCTCTC	CACCACTAGAATCTCTC
Ots_unk3513-49	C	T	TTTGAGTGAGTCACTGCACCAA	CAGCTCCACAGTGTCCACAT	AGTGCAGGAAGCC	AGTGCAGGAAGCC
Ots_unk7936-50	C	G	ATGGGTGGGATTATGTTCTATTG	CAAAATGGTTACTTGCATAGCTTTTGT	AGACATGTAGCTATGTAGTAA	AGACATGTAGCTATGTAGTAA
Ots_zn593-346	A	T	CTACGCGAGAAATAACACTTTTCAAACT	GGCGAGTTTATTACGGTGTATGAC	TCTTGCAATCAATTTTAA	CTTGCAATCAATTTTAA
Ots_u07-53.133	C	T	AGCTAGGCTGTAAATGCAAGGAT	CAGTGCTTCAATTCTGCTCAA	TAACACATGTTGGAGTC	AACACATGTTAGAGGTC
Ots_s146-516	C	A	TGTGTTTAGGATTGAATGACATGTT	CTAAACTCACTGCAAGGAAGGA	AACTAAGCGACTCC	TAGAACAATGACTGCTCC
Ots_unk9488-51	G	C	CAATCAGAACAAACCTCCACAA	GGAGCTGTCTGAATGGTGTCTT	CTCCCAACAACCC	TCGCCAACAACCC
Ots_U2362-330	A	G	AATGGGTAAACAAAGATAGCTAGTACTT	GACAGACCACAGTGAAGTGAAA	ACTGGGAAGATTGTTT	CTGGGAAGACTGTTT
Ots_RAS1	C	T	TCATAAATAGTGTCTTTTCACTAGTT	CTGACATGTGAATCACTAAGCTTTAATCAC	CAATCTATCATCGACGAGC	CAATCTATCATCGACGAGC
Ots_u07-20.332	A	C	CGGAGTGTAGCTGAATATTATGATTTC	TCAGCTAGCATAGCAACTTCATCAA	ACCATTGATATAACTGCGTTAG	CATTGATATAAGCGCGTTAG
Ots_u07-64.221	G	C	GAGGATGACACTGCTGTTTGT	CACAGTCTCTGATTACCTTGTAT	ATGCACCTGTCTATTAG	CGACCTGTGATTAG
Ots_ZR-575	G	A	GCCTACAGAAATACCAATTGTGA	ACTTTTCACTGTCTATTACAATTAGTATTTGATAT	CCGACACAATTTTGT	CCGACACAATTTTGT
Ots_GnRH-271	C	T	CAGATGAAAATAAATTTGGCCATTAGAA	CAGAGAGACTGAGACATATGATGTAGT	CAATGAATACATATCTAACCTAAT	AATGAATACATATCTAACCTAAT

Figure 9. Selecting species.

Additional Upload Options-

If you would like to save the markers that you are uploading as a unique marker set, one that you can select during data exporting, check the box labeled “Save Marker Set” and provide a name.

Selecting Fields-

Finally, select which columns contain the Marker Name, the VIC and FAM allele designations, the Forward Primer and Reverse Primer sequences and the VIC and FAM Probe sequences (Figure 10).

The screenshot shows the 'Upload markers' window with the following sections:

- Data Formatting:**
 - ☒ First row is Header
 - Select Delimiter: Tab
- Marker Configuration:**
 - Marker Type: SNP
 - Select Species: Oncorhynchus tshawytscha
- Additional Upload Options:**
 - ☒ Save Column Mapping
 - Column Mapping Name: SNP map
 - ☒ Save Marker Set
 - Marker Set Name: Tagman SNPs
 - Use Saved Column Mapping: [Select Mapping]

Below the configuration is a 'Toggle Fieldset View' button and a table with 7 columns. Each column has a dropdown menu to select the field to upload. The table contains 8 rows of marker data.

1	2	3	4	5	6	7
Marker Name	VIC Allele	FAM Allele	Forward Primer	Reverse Primer	VIC Probe	FAM Probe
Obs_1007-124	A	G	CGAATAAGGGCGCTGTGTTTAAA	TGTACGAGTGGAGCTTTGG	TGTCTGTCTCGAGATCA	CTGCAACTCGAGCGAAG
Obs_1046-123	G	A	CTGGTCTGTGAGCTCAAAATGATG	AGCTAGACCGAGGCTTTGAG	CTGCAACTCGAGCGAAG	CTGCAACTCGAGCGAAG
Obs_104-35	C	T	TAACCATGACTCTATCAATCAACCCG	CCTGCATACATGCTCAAACTGTG	CCACTAAGGATACGTTACG	CACTAAGGATACGTTACG
Obs_109-436	A	T	GCCCTGGAAGAGTACGTTTTAAACTAA	GCACCGATGTCAAGATTGCACATAA	CTAGGTGAAGCTTTTTTAAAA	CTAGGTGAAGCTTTTTTAAAA
Obs_1007	G	T	CTGCTGACCTGATGATGTTG	CCATGGTGGTCTGAGCAT	CCAGTGAAGGATG	CCAGTGAAGGATG
Obs_10035-171	G	T	ATGACCAATTGAAGAGTTCTTGGGT	CAAGGCGAAGCTGACATTAGACT	TTGATAATTGAAGGATTGA	GATAATTGAAGGATTGA
Obs_101363	A	T	GGTGATTTTGGCAGAGTAGAGAT	AGTTTAAATGTAAGCTGATACAGGGAAT	GGATGCTGTCTGTCTG	GATCTGTGATGCTG

Figure 10. Selecting fields during marker upload.

If you plan to upload multiple SNP definition files with the same column orders (e.g. Marker Name, VIC allele, FAM allele, etc.) you can check the box labeled “Save Column Mapping” and name it. This will allow you to select that saved column mapping in future uploads and skip the process of selecting fields.

Restriction site associated DNA (RAD) markers are SNPs adjacent to restriction enzyme recognition sequences. Similar to microsatellites and SNP markers, RAD marker names must be unique for every locus stored in the database. To ensure name uniqueness the following information must be included in the name of each RAD marker:

- Species
- Restriction Enzyme*
- LAB
- Project Number (this is a unique lab project identifier)
- SNP Position (This is the number counting from the start of the R.E. sequence to the SNP)
- Locus number

Etr Sbfl CRITFC 001 29 0001 (Species Restriction Enzyme LAB Project Number SNP Position Locus number).

This information also defines the locus and allows the database to check to make sure that the same name is not used for different alleles and the same allele sequence/SNP is not associated with different locus names. An example of a text file formatted to contain RAD marker name and definition information is shown below (Figure 11). The current marker definition file for RAD markers follows the "Miller" pipeline. We are in the process of adding functionality to the database to accommodate Stacks output (Catchen et al 2013).

CRITFC1_ERD_example - Notepad											
File	Edit	Format	View	Help							
Locus	Allele View (5'-3')										
	chr_SbIF1_CRITFC1_001_29	00001	Allele 2 (5'-3')	Restriction Enzyme	recognition site		SNP Allele 1	SNP Allele 2	SNP Position		
	chr_SbIF1_CRITFC1_001_29	00001					CCTCGAGGATGGTGAAGGTGAGACACCTGTCGCGCGGTGGCCAGTCGATCGTGGCAGGATCGGGC	SbIF1	CCTCGACGAG	T	6
	chr_SbIF1_CRITFC1_001_29	00002					CCTCGAGGCAAAAGTGGGGGCGACACAACTTTTGTTTGTAATGATGACATTCATTCGATTTGTTGA	SbIF1	CCTCGACGAG	T	29
	chr_SbIF1_CRITFC1_001_40	00003					CCTCGACGGCTCTGCTCGCTATGCGATCTTTTGTCGCATCTTCTGCCGACGGCTGGGCTTTGGATAT	SbIF1	CCTCGACGAG	A	6
	chr_SbIF1_CRITFC1_001_40	00004					CCTCGACGGCTCTTCTCTGCTGCTAGAGTGTACGCGCAATCTGGGATACACCGGCTCTCAGGAATGAA	SbIF1	CCTCGACGAG	T	40
	chr_SbIF1_CRITFC1_001_40	00005					CCTCGAGGGTGGCTCAAGGTGAACAAAAATAACGACAGATATTTTATTTTACAGTAAAGAAC	SbIF1	CCTCGACGAG	T	40
	chr_SbIF1_CRITFC1_001_64	00006					CCTCGAGAGAGCTCTGGCTGCTCTCCAGCTGGCTCGCAAGGCGCTGGCTCTGTCGACGAACAAACA	SbIF1	CCTCGACGAG	A	64
	chr_SbIF1_CRITFC1_001_65	00007					CCTCGAGGTGAACCCGCGCCGACACCGCGCACTTGTTGCTCTGCTGGGCGAGGACGCG	SbIF1	CCTCGACGAG	T	65
	chr_SbIF1_CRITFC1_001_38	00008					CCTCGAGGGGCTCGACCTTTTGGATGAGTGTGTCACCTGGCTGCTGCTGTAAGGCACCGGGGG	SbIF1	CCTCGACGAG	T	38
	chr_SbIF1_CRITFC1_001_48	00009					CCTCGAGAGAGTCTGAGGCTGGAACCTGACGGGGGCTGGTGTGCTGCTGAGGACCTGCTAGGCGA	SbIF1	CCTCGACGAG	C	48
	chr_SbIF1_CRITFC1_001_39	00010					CCTCGAGAGCTCGCGAGATCTTTCGCTGCGACGATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTG	SbIF1	CCTCGACGAG	T	39
	chr_SbIF1_CRITFC1_001_17	00011					CCTCGAGAGCAGCTGCTGGGATCTGGGCGACAGGGGAGAGGCTGCTGGTAGGAGATGCTGGTGGTGA	SbIF1	CCTCGACGAG	T	17
	chr_SbIF1_CRITFC1_001_40	00012					CCTCGAGATTAAGTGAAGCGTAAGGCGACCTGACCTATTTCTAGCATCTGATGGGCGATGGGTTG	SbIF1	CCTCGACGAG	C	40
	chr_SbIF1_CRITFC1_001_40	00013					CCTCGAGAGAGTGTGGTGTCTATGTCATCGATCTGACGCCAGCTGATATTTGAATCTTGCCTGGT	SbIF1	CCTCGACGAG	T	6
	chr_SbIF1_CRITFC1_001_40	00014					CCTCGAGAGTACATTTTGAAGAGCGGAAGAGCTGCTCAAGTGGCGTGATGATTAATGATCGATTAAT	SbIF1	CCTCGACGAG	A	40
	chr_SbIF1_CRITFC1_001_53	00015					CCTCGAGGCGTAGGCTGAGGTGATGAGTCAAGGAGAGAGTGGGAATAGGAGCTATGCCACACGCTAT	SbIF1	CCTCGACGAG	C	53
	chr_SbIF1_CRITFC1_001_34	00016					CCTCGAGAGCTGCTGACGACAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	SbIF1	CCTCGACGAG	T	34
	chr_SbIF1_CRITFC1_001_34	00017					CCTCGAGGGTCTGCGACATGAGGACGACGAAGGGCTCATGCAATGTAGGAGTTGACGAGTGGGGGG	SbIF1	CCTCGACGAG	C	34
	chr_SbIF1_CRITFC1_001_48	00018					CCTCGAGGCTCACGATCCGCTCTCCAGGCTCATCTCTGGGGGGCTCGGCGGGGACACACGACGGA	SbIF1	CCTCGACGAG	T	48
	chr_SbIF1_CRITFC1_001_38	00019					CCTCGACGAGGACCTGGAAGGACGACGAGTGGTATGGTGAATTAATGCAATAGAGGCTTGGCGA	SbIF1	CCTCGACGAG	A	38
	chr_SbIF1_CRITFC1_001_49	00020					CCTCGAGGGCGGCTCTTGGAGGCGACGACGAGCTCGCGGAGAGGCGGCGGCTCTCTCCGTCGATCT	SbIF1	CCTCGACGAG	T	49
	chr_SbIF1_CRITFC1_001_40	00021					CCTCGACGGCAGCTCTCACTACTACTGCTGACGCTGCAACAGAGCGAGGAGGACAGAGCGGCTCTC	SbIF1	CCTCGACGAG	C	40
	chr_SbIF1_CRITFC1_001_40	00022					CCTCGACGGCGCTGGAGCGCCCTCTCAAGTCCGCTCTGGCTCTCAGCAGATCTGTGACCTCTCTCTC	SbIF1	CCTCGACGAG	A	40
	chr_SbIF1_CRITFC1_001_40	00023					CCTCGAGGCGCGGCTCGACGCTCCGACACCGACCCGACGCTCTCTCTCTCTCTCTCTCTCTCTG	SbIF1	CCTCGACGAG	C	40
	chr_SbIF1_CRITFC1_001_20	00024					CCTCGAGGGTGAATGCTCAACCCGACACCGCTGATCTTTGAGGCGGATGACGATCAGGGAGATC	SbIF1	CCTCGACGAG	G	31

Figure 11. Text file formatted to contain RAD marker name and definition information. *The restriction enzyme sequence must also be included in the text file, but is not required in the name.

After the text file has opened, you will need to provide the following information:

Data Formatting-

- Check the box if the first row in your marker definition file is a header row.
- Select the delimiter (tab, comma, or space)

Marker Type-

- Select RAD

Select Species-

- Select species that the RAD marker is screened on.

1	Locus	Marker Name
2	Allele_1 (5'-3')	Sequence A
3	Allele_2 (5'-3')	Sequence B
4	Restriction Enzyme	Restriction Enzyme
5	recognition site	Recognition Site
6	SNP Allele 1	Snp Allele A
7	SNP Allele 2	Snp Allele B
8	SNP Position	Snp Position

Figure 12. Text file formatted to contain RAD marker name and definition information.

Additional Upload Options-

If you would like to save the markers that you are uploading as a unique marker set, one that you can select during data exporting, check the box labeled “Save Marker Set” and provide a name.

Selecting Fields-

Finally, select which columns contain the Marker Name, Allele 1 and Allele 2 sequence (minimum of 50 b.p., maximum of 99 b.p.), recognition site sequence (e.g. SbfI = CCTGCAGG), SNP allele 1, SNP allele 2, and SNP position. The recognition site sequence must be included at the left (5') end of the allele. With this information, FishGen will check Marker Names, allele sequences, allele designations and SNP positions to ensure Marker standardization. This prevents different RAD marker from being uploaded into FishGen under the same name and prevents the same SNP being uploaded under different marker names.

Uploading genetic data

Once the genetic markers in your dataset have been defined and uploaded in FishGen, you can upload a data file that contains metadata and genetic data from a dataset. Metadata is captured within Collection Fields and Individual Fields. Collection fields contain information that applies to all individuals within the collection. Within a collection field, all of the data must be the same for all rows. Individual fields contain information unique to an individual fish. Fishgen only requires that seven collection fields are completed and three individual fields are completed. A complete list of possible fields and valid entries for each field is available in the Appendix (A and B).

Required Collection Fields-

Body of Water: The river, stream, creek, lake, pond, ditch, etc. that your sample came from.

FishGen will automatically calculate HUC8 designations, so additional details regarding drainage, basin, etc. are not needed.

Hatchery: The hatchery your samples came from.

Collection Species: Genus species. Must be written out completely and spelled correctly. The term "Mixed" can be used for hybridization studies that involve sampling multiple species. However, Mixed is not intended to be used outside of hybridization studies (e.g. you wouldn't include a sample of steelhead and Chinook salmon under the same collection).

Collection Origin: Whether the collection consists of wild, hatchery or a mixture of wild and hatchery fish.

Sample Year: In what year (e.g. 2013) or range of years (e.g. 2013 – 2014) did the samples in your collection come from.

Collection Latitude and Longitude: Collection latitude and longitude are extremely important, since FishGen will calculate and autopopulate State/Province and USGS Hydrological Unit Code (HUC) information for your collection. Collection Latitude and Longitude must be the same for all individuals in the collection. In a situation where you have sampled multiple locations within a stream, individual latitude/longitude coordinates can be entered at the individual level. **Please see section below titled: "Entering Latitude and Longitude coordinates for your dataset".**

Collection Name: A name that describes each collection of samples. We recommend that these names are descriptive, since each collection name must be unique in FishGen and is limited to 30 characters. One example might be OmyOXBO08, which combines information on species, sample location, and sample year.

Required Individual Fields-

Individual Name: A name that describes each collection of samples. We recommend that these names are descriptive, since each name must be unique in FishGen and is limited to 30 characters. One example might be OmyOXBO08, which combines information on species, sample location, and sample year.

Phenotypic Sex: This information is useful for Parentage Based Tagging programs. Valid fields are: F = Female; M = Male; U = Unknown

Phenotypic Species: A list of valid species is provided in the appendix.

Valid Genetic Data-

Microsatellites

- The allele values can be in 2-digit or 3-digit format: 01-99 or 001-999
- Alleles can't be >999
- X, Y for sex marker
- 0, 00, or 000 could be input for no data
- Can't have blank cells
- Can't have one allele with 0 and the other allele >0
- Can't have any other text than X, Y
- Text and numbers cannot go together (e.g. X, 0)

SNP and RAD data

- Alleles can be in numeric or alpha characters.
- For alpha characters, allele values are A, C, G, T, X, Y, 0, or -
- For numeric values we follow the HapMap standard: A = 1, C = 2, G = 3, T = 4, - = 5
- For sex markers, use X = 6 and Y=7
- 0 is no data

Entering Latitude and Longitude coordinates for your dataset

As mentioned above, entering accurate estimates of Latitude/Longitude coordinates for sample collections is important, because the database will map these collections and estimate Hydrological Unit Codes (United States) and/or Watershed Groups and Watershed names (Canada) for collections and auto-populate these values within the database. Although it is encouraged that users require samplers to measure latitude/longitude coordinates in the field with a GPS unit, the database does allow users to locate sample locations on ESRI map layers and cut and paste latitude/longitude values. The database also allows users to enter latitude/longitude coordinates and zoom in to see the point on an ESRI map for verification purposes.

Find latitude/longitude coordinates for a collection:

To find latitude/longitude coordinates, simply use the available map layers on the search page and the coordinate widget (Figure 13) to place a pin on the map and obtain Latitude and Longitude coordinates that can be copied and pasted into a text file. To activate the pin, click your mouse once. This will place a pin on the map and show the latitude and longitude coordinates in the coordinate box.

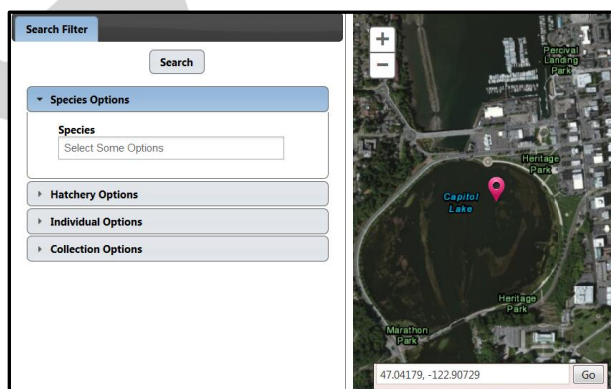


Figure 13. Coordinate widget for placing a point on the map. The pin is red (next to Capital Lake).

Verify latitude/longitude coordinates for a collection:

To find verify that the latitude/longitude coordinates you have associated with a collection are accurate, simply cut and past the coordinates into search box in the bottom left of the screen (latitude,longitude) and press “Go” (Figure 14). Then use the map layers and the zoom (+) button to identify where coordinates currently map your collection.

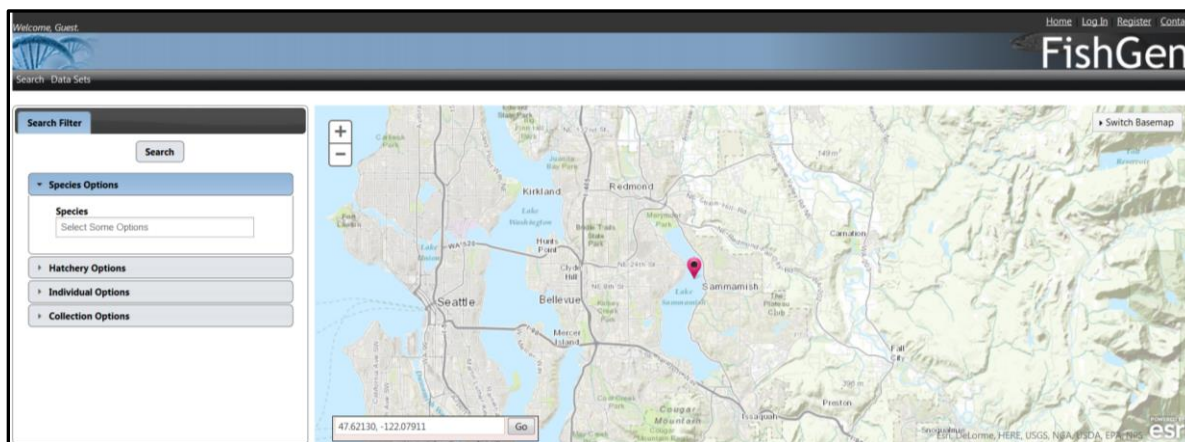


Figure 14. Verifying latitude/longitude coordinates.

Uploading Collections-

To upload a text file that contains meta- and genetic collection data you can either select “Upload Data” below the SNP plot on the home page or select “Contributor” from the header line and select “Upload Collections” from the drop-down (Figure 15).



Figure 15. Upload collections from the Contributor dropdown.

This will bring you to the Upload Collection Page (Figure 16), where you can Browse for your text file saved on your computer.

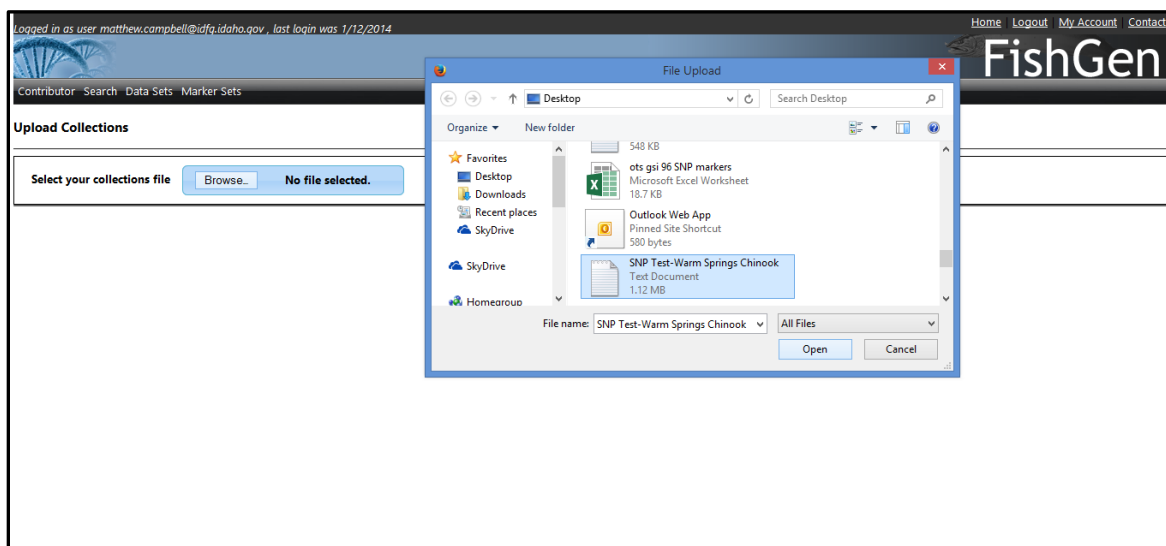


Figure 16. Browse for text file containing collection information.

After selecting your file and pressing “Open”, FishGen will bring up your file in the Upload Collections window (Figure 17).

Upload Collections

Upload Cancel

Data Formatting

Select Delimiter: Tab

Column Number Where Genetic Data Begins:

☒ Genetic data is in 2 columns

☐ SNP genetic data is numeric

Allele Suffix Configuration

Allele 1 Suffix Pattern:

Allele 2 Suffix Pattern:

Preview Marker Name:

Additional Upload Options

☐ Data is Private

☐ Save Column Mapping

☐ Save Data Set

Use Saved Column Mapping: [Select Mapping]

Toggle fieldset View

1	2	3	4	5	6
<Ignore Field>	<Ignore Field>	<Ignore Field>	<Ignore Field>	<Ignore Field>	<Ignore Field>
BPA project	Body of Water	Hatchery	Collection Species	Phenotypic Species	Collection Name
2009-018-00		Warm Springs NPH	Oncorhynchus tshawytscha	Oncorhynchus tshawytscha	Warm Springs NPH_1575
2009-018-00		Warm Springs NPH	Oncorhynchus tshawytscha	Oncorhynchus tshawytscha	Warm Springs NPH_1575
2009-018-00		Warm Springs NPH	Oncorhynchus tshawytscha	Oncorhynchus tshawytscha	Warm Springs NPH_1575
2009-018-00		Warm Springs NPH	Oncorhynchus tshawytscha	Oncorhynchus tshawytscha	Warm Springs NPH_1575

Figure 17. Upload Collections Window

After the text file has opened, you will need to provide the following information:

Data Formatting-

- Select the delimiter (tab, comma, or space)
- Identify the column number where the genetic data begins. This would be the first column that follows metadata fields.
- FishGen accepts genetic data in 1 or 2 column format. The default is 2 columns and the box is checked automatically. If your data is in 1 column format, uncheck the box.
- FishGen accepts genetic data in numeric or letter format: A = 1, C = 2, G = 3, T = 4, - = 5, X = 6, and Y = 7. The default is letter format. If your data is in numeric format, check the box.

Allele Suffix Configuration-

- Marker names must include a suffix differentiating allele 1 from allele 2. Some examples include: _1/_2; -A/-B; L/R; etc. Please indicate what configuration is used. Pressing the “Preview Marker Name” button should show the marker name in the first column where the genetic data begins. The name shown will not include the allele suffix.

Additional Upload Options-

- Genetic data that is uploaded to FishGen can either be made immediately available to the public or stored privately for up to 6 months. The 6 month time period is intended to allow the user to meet project/reporting requirements while preparing data for publication. If the “Data is Private” box is checked, FishGen will withhold the release of the submission for up to 6 months. During this period, the user may delete the uploaded collections without contacting the curator. The user will be notified via e-mail, 1 month and 1 week prior to the due date. After 6 months, the submission will be made public.
- “Column mapping” refers to association of column headings in the uploader’s text file with the appropriate collection and individual fields used in the database. This process will be somewhat time consuming, especially if you are new to the database and have many metadata fields. To make this process faster for future uploads, the user can save the column mapping configuration and then use that saved configuration to map additional collection uploads. To use this feature, check the “Save Column Mapping” box and name it. On future uploads, after the text file has been uploaded, select the appropriate Column Map from the dropdown and the database will automatically fill in the correct column headings.
- The “Save dataset” feature allows the user to save the collections that are being uploaded into a separate stored file. **It is critical that the user understands that “Saved Datasets” are snapshots of collections (meta and genetic data) stored in the database. Any subsequent changes that might occur in the source database will not be reflected in “Saved Datasets”.** We envision that “Saved Datasets” will include such things as a completed PBT baseline that will be used for analyses and reporting purposes during a particular return year. In these situations, the uploader will likely e-mail collaborators with the name and description of the saved dataset. Another example of a “Saved Dataset” may be a collection of samples and genetic data that are part of a published manuscript. For example, FishGen currently contains metadata and genetic data for all 15,658 individuals as part of the Blankenship et al 2011 paper examining major steelhead lineages and metapopulations in Columbia River basin.

Searching for saved datasets and collections

Saved Datasets-

The easiest way to search for genetic collections stored on FishGen is from the home page, under the heading “Data Sets” and then the dropdown “Find and export” (Figure 18).

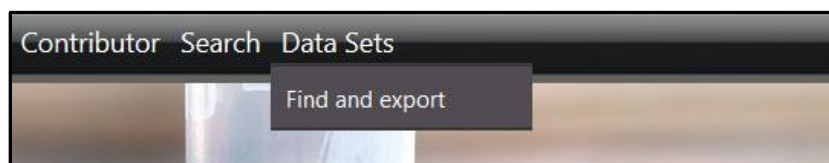


Figure 18. Find and export saved datasets.

This will take you to the “Data Set Find and Export” page (Figure 19). From here you can search by Dataset Name, Species, Organization, or BPA project number. If you know the name of the saved dataset you are interested in (e.g. Blankenship et al 2011), typing this name into the “Name” box and hitting the Search button will bring the dataset up in the Search Results window. From here, you can press the “Notes” button to read a brief summary of the saved dataset or you can Export the dataset. Currently, collections and datasets in FishGen can be exported in GenePop format or IDFGen format. Details of these formats are described below:

Dataset Name	Private	Dataset Owner	Organization	# of Collections	# of Individuals	Notes
Blankenship et al 2011	<input type="checkbox"/>	Matthew Campbell	Idaho Department of Fish and Game, Eagle Fish Genetics Lab, Eagle, ID	344	15658	Standardized microsatellites Export Delete

Figure 19. Data Set Find and Export page.

IDFGen format details:

- Tab-delimited .txt file
- First row always contains column header names
- One row per individual
- First column always contains some sort of population/collection identifier
- Second column always contains some sort of unique individual identifier
- Columns 3 through # are collection/individual level fields, whichever are selected by the user for exporting. The number of fields exported is flexible.
- All columns after the last collection/individual level field contain genetic data:
- Two columns per marker (regardless of marker type)
- SNP and RAD data:
 - VIC/Allele A in the first column

- FAM/Allele B in the second column
- uSAT data:
 - Three-digit numbers or 000 for no Call.
 - First Allele in the first column
 - Second allele in the second column

Genepop format details:

- Tab-delimited .txt file
- First row contains the title line or any use line
- The second row contains the names of loci, separated by commas
- The first row after locus names contains the word: Pop (no case sensitivity). This is also used as a header each time a new population is started.
- Rows following “Pop” include the sample name, alleles at each locus, separated by a space between loci (missing data should be indicated with 0, not a blank).
- The exported Genepop file can be cut and pasted directly into Genepop on the web for analyses or can be uploaded into Genalex for analysis or additional conversion to other software formats.



Searching for collections-

When not looking for saved datasets, the database can be searched for available collections by selecting the “Search” tab from the toolbar. This will bring up the Search Page (Figure 20), where you can search for collections using several filters and sub-options. The primary filter options include Species, Hatchery, Individual, and Additional Collection.

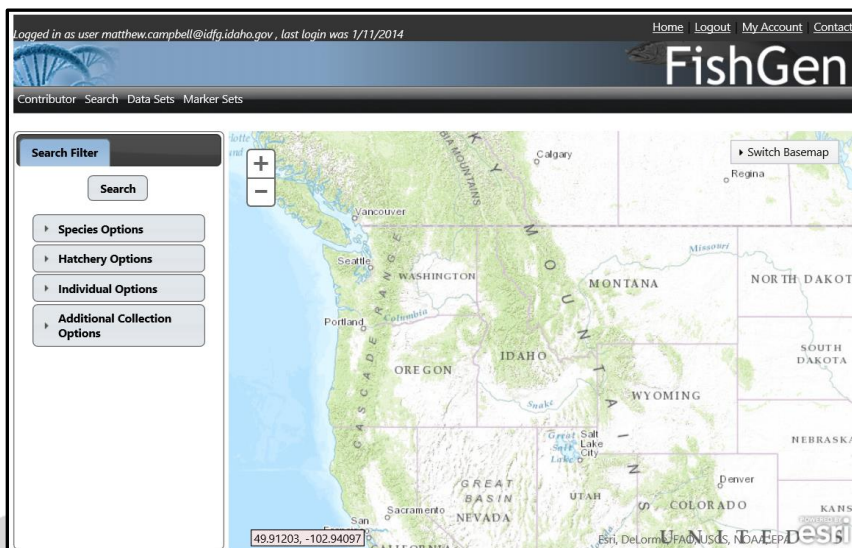


Figure 20. Search page.

Under species, only species that have actually been uploaded into FishGen are shown (Figure 21).

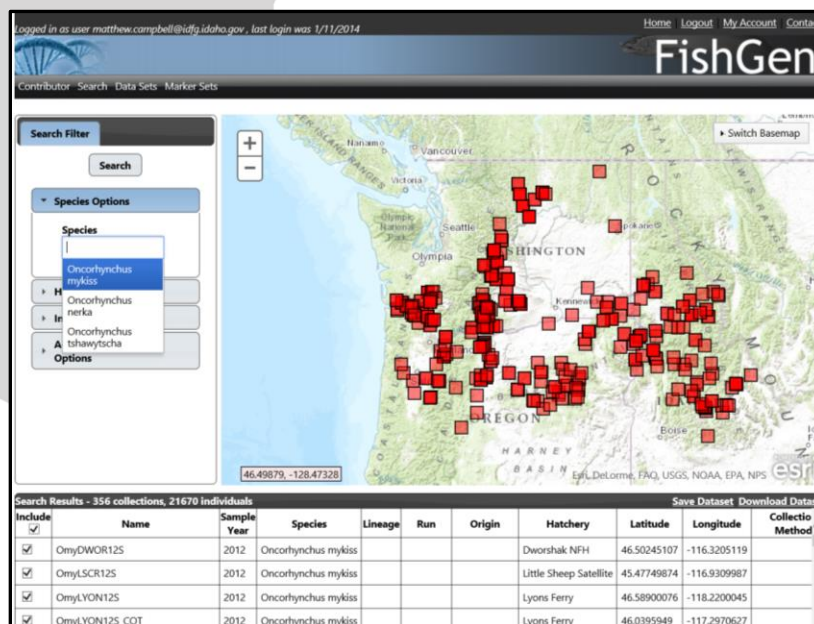


Figure 21. Filtering by species.

Under “Hatchery options”, several sub-options are available including: Hatchery States, Hatchery, Funding Source and Organization. Selecting the “Hatchery States” sub-option will show you all States that currently have hatcheries represented in the database. After selecting a State and pressing “Search”, all hatchery collections present in the database from that State are shown on the map (Figure 22). Clicking a collection box (red) will bring up a bubble that provides information about that collection including: Name, sample size, sample year, species, region, subregion, basin, subbasin.

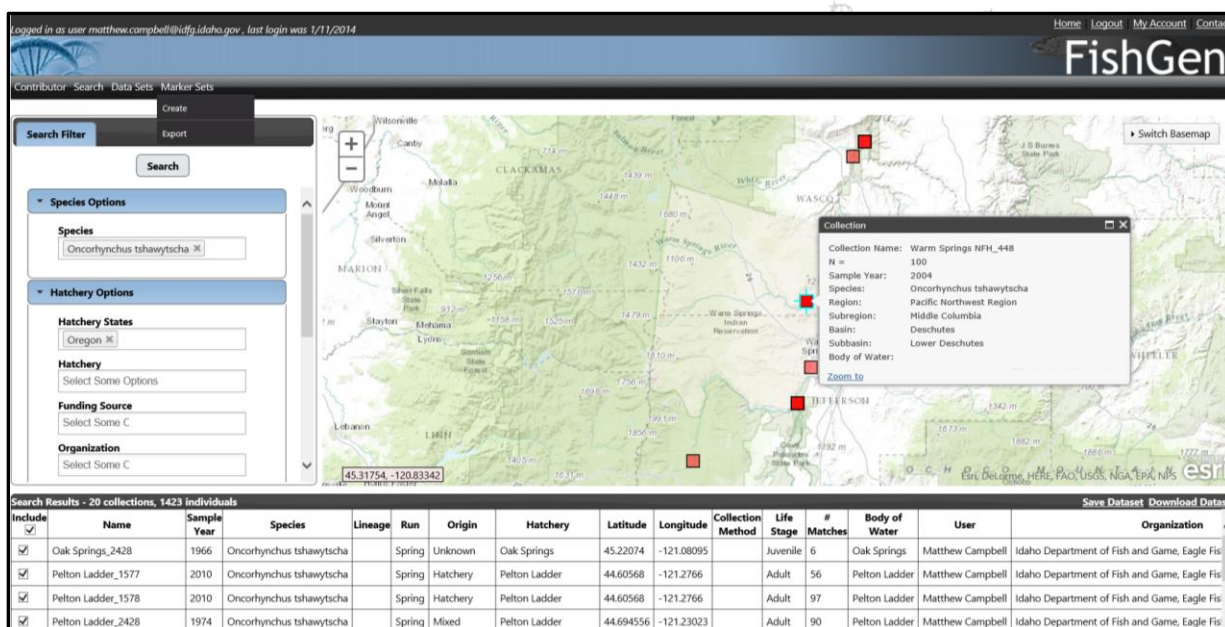


Figure 22. Filtering by hatchery collections.

Under “Individual options”, several sub-options are available including: Phenotypic Sex, Life Stage, and Origin. In addition to these sub-options, several check boxes are also included: Has Pit Tag, Has CWT Tag, Has Jaw Tag and Has Floy Tag.

Finally, under “Additional Collection Options”, the following sub-options are available: Sample Year range search, HUC4, and BPA Projects.

Appendix A. Collection Fields

	Body of Water	Hatchery	Country	State/Province	HUC 2 (Subregion)	HUC 4 (River Basin)	HUC 6 (Subbasin)	HUC 8 (Watershed)	HUC Number
Required?	YES (if hatchery is not selected)	YES (if Body of Water not selected)	YES-Auto	YES-Auto	YES-Auto	YES-Auto	YES-Auto	YES-Auto	YES-Auto
Description/ Definition	The river, stream, creek, lake, pond, ditch, etc. that your sample came from. FishGen will automatically calculate HUC8 designations, so additional details regarding drainage, basin, etc. are not needed.	The hatchery your sample came from. FishGen will automatically calculate HUC8 designations, so additional details regarding drainage, basin, etc. are not needed.	These fields are all auto-generated from user provided latitude/longitude coordinates.						
Example	Seven Suckers Ditch	Dworshak National Fish Hatchery	Canada	Oregon	Pacific Northwest Region	Middle Columbia	Deschutes	Upper Deschutes	17070301
Valid Entry	Alphanumeric, 30 character limit	See Hatchery Tab	AUTO	AUTO	AUTO	AUTO	AUTO	AUTO	AUTO

Appendix A. Collection Fields (continued)

	BPA Project Number	Collection Species	Collection Comments	Collection Run	Collection Origin	Collection Life Stage	Collection Method
Required?	NO	YES	NO	NO	NO	NO	NO
Description/ Definition	If genetic data uploaded to FishGen was generated as part of a Bonneville Power Administration Project, you can provide your project number for reporting requirements.	Genus species Must be written out completely and spelled correctly. The term "Mixed" can be used for hybridization studies that involve sampling multiple species. However, Mixed is not intended to be used outside of hybridization studies (e.g. you wouldn't include a sample of steelhead and Chinook salmon under the same collection)	Field or lab comments that apply to the entire collection.	Runs have been identified on the basis of when adult salmon enter freshwater to begin their spawning migration.	Whether the collection consists of wild, hatchery or a mixture of wild and hatchery fish.	Life Stage of the collection. For collections that include fish of multiple life stages, please use "Mix".	How samples were collected. Names must match exactly from the list above. (e.g. Electroshocking will not work for Electrofishing). A collection method not listed (e.g. noodling), can be requested from the curator.
Example	2010-026-00	Oncorhynchus tshawytscha	Samples were collected on private property (Eagle Island State Park)	Summer	W	Adult	Electrofishing
Valid Entry	0000-000-00	See "Species" tab	Alphanumeric	Spring, Summer, Fall, Winter, Unknown, Resident	H = Hatchery W= Wild Mix = Mixture of hatchery and wild U = Unknown	Adult, Carcass, Egg, Fry, Juvenile, Larvae, Mix, Parr, PreSmolt, Smolt, Unknown	Angling, Bait Trap, Captive Brood, Carcass Survey, Creel, Egg-box, Electrofishing, Fish Ladder at Dam, Gill net, Hatchery Sample, Multiple, Other, Outmigrants, Redd Pump, Screw trap, Seine, Snorkel, Trawl, Unspecified, Weir

Appendix A. Collection Fields (continued).

	Sample Year	Collection Latitude	Collection Longitude	Collection Name
Required?	YES	YES	YES	YES
Description/ Definition	The year in which samples were collected. Generally samples collected from different years should be separated into unique collections. For samples spanning across years, like samples taken at a weir or dam, the range can be input (e.g. 2010-2011)	Collection latitude and longitude are extremely important, since FishGen will calculate and auto-populate HUC information for your collection. Collection Latitude and Longitude must be the same for all individuals in the collection. In a situation where you have sampled multiple locations within a stream, individual lat/lon coordinates can be entered at the individual level		Collection Name from uploader. We suggest that these are descriptive. Ours include: Species: Omy Sample location: Oxbow (OXBO) Sample year: 08 Remember that Collection Names are unique in the database. So they must be unique enough that they don't match another collection, but they need to stay under the 30 character limit.
Example	2013	43.67731	-116.40309	OmyOXBO08S
Valid Entry	YYYY	These must be input as decimal degrees	These must be input as decimal degrees	Alphanumeric, 30 character limit

Appendix B. Individual Fields.

	Ad Clip	Brood Year	Brood Year Determination Method	Cross Data	CWT Number	Date Spawned	Disposition 1	Disposition Year 1
Required?	NO	NO	NO	NO	NO	NO	NO	NO
Description/ Definition	Whether the adipose fin was clipped or not. A clipped adipose fin is an indication that it is a hatchery fish.	A brood year is the year of spawning of the parental generation, e.g., an juvenile produced from parents spawned in 2013 is a brood year 2013 (BY13) fish	How was brood year determined, a physical tag, PBT assignment? Or was it estimated via length?	This is for broodstock sampled at a hatchery. Documents which fish it was spawned with.	Binary or alpha-numeric code that identifies a specific stock or release group	Sometimes the date that a fish is spawned differs from the date it was trapped/sampled.	The history of a fish following genetic sampling. Useful for PBT tracking, spawning programs, and for situations where fish are released following sampling.	Year in which the event occurred.
Example	Y	2013	PBT assignment	OmyOXBO08S	10110	7/19/2013	Spawned	2013
Valid Entry	N = No P = Partial U = Unknown Y = Yes	yyyy	Alphanumeric, 300 character limit	semi-colon separated alphanumeric	Alphanumeric, 30 character limit	mm/dd/yyyy	ARtoCB, Carcass, CBtoAR, Culled, CulledBKD, CulledHybrid, CulledIHN, CulledSurplus, EggsCulled, Immature, Killed, Maturing, Mort, NonProductiveSpawner, NotInMatrix, NotSpawned, OffSeasonMaturity, Poned, Precocial, Released, RelAboveWeir, RelBelowWeir, RelAnotherLoc, ReUsed, Spawned, Unknown	yyyy

Appendix B. Individual Fields (continued).

	Disposition 2	Disposition Year 2	Field ID 1	Field ID 2	Floy Tag Number	Sex (Genetic)	Sex (Phenotypic)	Hatchery Database ID
Required?	NO	NO	NO	NO	NO	NO	YES	NO
Description/ Definition	A secondary disposition for individuals. Important in cases where a fish is used for hatchery spawning, and then released back in the wild to spawn naturally. In this case Disposition1 would be 'Spawned' and Disposition2 would be 'ReleasedAboveWeir' or something similar.	Year in which the event occurred.			Binary or alpha-numeric code that identifies a specific stock or release group	Determined from running a genetic sex marker	What sex was the fish?	Unique number from the LSRCF FINS hatchery database
Example	Spawned	2013	F_001	F_001	FT12345	F	F	FINS_DWOR_13_0001
Valid Entry	ARtoCB, Carcass, CBtoAR, Culled, CulledBKD, CulledHybrid, CulledIHN, CulledSurplus, EggsCulled, Immature, Killed, Maturing, Mort, NonProductiveSpawner, NotInMatrix, NotSpawned, OffSeasonMaturity, Poned, Precocial, Released, RelAboveWeir, RelBelowWeir, RelAnotherLoc, ReUsed, Spawned, Unknown	YYYY	Alphanumeric, 30 character limit	Alphanumeric, 30 character limit	Alphanumeric , 30 character limit	F = Female M = Male U = Unknown	F = Female M = Male U = Unknown	Alphanumeric, 30 character limit

Appendix B. Individual Fields (continued).

	Individual Comments	Individual Latitude	Individual Longitude	Latitude/Longitude Notes	Individual Name	Jaw Tag Number	LAB ID 1	LAB ID 1	Length FORK (mm)	Length MEHP (mm)
Required?	NO	NO	NO	NO	NO	NO	NO	NO	NO	NO
Description/ Definition	Individual comments related to the fish or the genetic sample taken from the fish	In a situation where you have sampled multiple locations within a stream, lat/lon coordinates can be entered at the individual level.		Notes about lat/lon coordinates	Specific name lab uses to identify sample, must be unique for all individuals within a collection	Binary or alpha-numeric code that identifies a specific stock or release group	LAB specific ID number	LAB specific ID number	Fork length is the length from the most anterior part of a fish to the tip of the median caudal fin rays.	Mid-eye to end of hypural plate
Example	Fungused fin	43.67731	- 116.40309	Estimated at mouth	OmyOXBO08S_001	JT101	101035	Plate-0304B	510	475
Valid Entry	Alphanumeric, 300 character limit	These must be input as decimal degrees	These must be input as decimal degrees	Alphanumeric, 300 character limit	Alphanumeric, 300 character limit	Alphanumeric, 30 character limit	Alphanumeric, 30 character limit	Alphanumeric, 30 character limit	Numeric (must be in millimeters)	Numeric (must be in millimeters)

Appendix B. Individual Fields (continued).

	Length POH (mm)	Length TOTAL (mm)	Life Stage	Life Stage Determination Method	Lineage	Offspring Reared Hatchery	Offspring Release Strategy	Opercle Punch
Required?	NO	NO	NO	NO	NO	NO	NO	NO
Description/ Definition	Post-orbital hypural length	Total length is the measurement of the entire length of a fish's body, from the most anterior part of the fish to the tip of the longest caudal fin rays	A series of stages a fish follows as it develops from an egg to an adult	How was the life stage determined? A tag or physical attribute or measurement?	Lineage names and descriptions are not consistently used among biologists, managers or geneticists and they are not defined strictly by geography or run-timing. However, several are commonly used to describe salmon and steelhead populations throughout the PNW.	Used to designate where an adult's offspring will be raised.	Used to designate the release strategy of an adult's offspring	Does the fish have an opercle (gill cover) punch? This usually indicates that this fish is of hatchery origin
Example	350	575	Adult	Smolts were defined as fish with a silver coloration and a fork length >110 mm	Chinook - Lower Columbia	Magic Valley Fish Hatchery	Presmolt	Y
Valid Entry	Numeric (must be in millimeters)	Numeric (must be in millimeters)	Life Stage, Adult, Carcass, Egg, Fry, Juvenile, Larvae, Parr, PreSmolt, Smolt, Unknown	Alphanumeric, 300 character limit	Alphanumeric, 30 character limit. Suggested names are: Chinook - Lower Columbia, Chinook – Ocean, Chinook – Stream, Steelhead – Interior, Steelhead – Coastal, Mixed, Unknown	See Hatchery Tab	Alphanumeric, 30 character limit	N = No P = Partial U = Unknown Y = Yes

Appendix B. Individual Fields (continued).

	Origin	PIT Tag Number	Individual Run	Sample Date	Species (Phenotypic)	Species (Genetic)	Stock Strain	Ventricle Clip
Required?	NO	NO	NO	NO	YES	NO	NO	NO
Description/ Definition	Is the fish of hatchery or wild origin?	Binary or alpha-numeric code that identifies a specific stock or release group	Runs have been identified on the basis of when adult salmon enter freshwater to begin their spawning migration.	What day was the fish sampled?	What species is the fish you sampled?	Expectation is that this would match phenotypic species, unless genetics indicated otherwise. For example, a rainbow trout was identified in the field, but was determined to be an F1 Hybrid.	In this database, stocks are common names ascribed to individual spawning populations.	Whether the ventral (right or left pelvic fin) has been clipped or not. A clipped fin is an indication that it is a hatchery fish.
Example	H	3D9.1C2D1238F4	Summer	7/19/2013	Oncorhynchus tshawytscha	Oncorhynchus tshawytscha	Skamania	N
Valid Entry	H = Hatchery W = Wild Mix = Mixture of hatchery and wild U = Unknown	Alphanumeric, 30 character limit	Spring, Summer, Fall, Winter, Unknown, Resident	mm/dd/yyyy	See "Species" tab	See "Species" tab	Alphanumeric, 300 character limit	N = No P = Partial U = Unknown Y = Yes

Appendix C. Hatcheries

Abernathy Fish Technology Center (USFWS)	Chewuch Pond	Eagle Creek NFH
Alsea Hatchery	Chief Joseph	Eagle Fish Hatchery
American River Trout Hatchery	Chinook River / Sea Resources	East Fork Satellite
Bandon Hatchery	Chiwawa Pond	Eastbank
Beaver Creek	Clackamas	Easton Satellite
Big Canyon Satellite (NPT)	Clark Flat Satellite	Elk River Hatchery
Big Canyon Satellite (ODFW)	Cle Elum SRF	Elochoman
Big Creek	Clearwater	Elwha Channel
Big Qualicum Hatchery	Cole M. Rivers Hatchery	Entiat NFH
Birnie Creek (FFA)	Coleman National Fish Hatchery	Fall River Hatchery
Bonapart Pond	Cottonwood Creek Pond	Fallert Creek
Bonifer Pond	Cowlitz Salmon	Feather River Hatchery
Bonneville	Cowlitz Trout	Feather River Hatchery-Thermalito An
Burley Creek (Safety-Net)	Coyote Valley Fish Facility	Fillmore Trout Hatchery
Capt John Rapids Satellite	Crystal Lake Trout Hatchery	Forks Creek Hatchery
Carlton Pond	Curl Lake Ponds	George Adams Hatchery
Carson NFH	Darrah Springs Trout Hatchery	Gnat Creek Hatchery
Cascade Hatchery	Dayton Ponds	Gobar Pond
Catherine Creek Satellite	Deep River Net Pens	Grays River Hatchery
Cedar Creek Hatchery	Dexter Ponds	Hagerman ARI
Cedar Flats Satellite	Dryden Ponds	Hagerman NFH
Chelan	Dworshak NFH	Hot Creek Trout Hatchery

Appendix C. Hatcheries (continued).

Hupp Springs Rearing Ponds	Little Sheep Satellite	Minter Creek Hatchery
Hurd Creek Hatchery	Little White Salmon NFH	Minthorn Springs Satellite
Imeques Satellite	Livingston Stone National Fish Hatchery	Minto Fish Collection Facility
Imnaha Satellite	Lookingglass	Moccasin Creek Trout Hatchery
Iron Gate Hatchery	Lostine Satellite	Mokelumne River Hatchery
Irrigon Hatchery	Lower Crooked River Satellite	Morse Creek Hatchery
Jack Creek Satellite	Lukes Gulch Satellite	Mount Shasta Trout Hatchery
Kalama Falls Hatchery	Lummi Bay Complex	Nehalem Hatchery
Kendall Creek Hatchery	Lyons Ferry	Newsome Creek Satellite
Kern River Trout Hatchery	Mad River Hatchery	Nez Perce Tribal
Kingfisher Flat Fish Facility (Big Creek Hatchery)	Magic Valley	Niagara Springs
Klamath Hatchery	Manchester Marine Laboratory	Nimbus Fish Hatchery
Klaskanine Hatchery	Marblemount Fish Hatchery	North Lapwai Valley Satellite
Klickitat Fish Hatchery	Marion Drain Hatchery	North Toutle Hatchery
Kooskia NFH	Marion Forks Hatchery	Oak Springs
Lake Wenatchee Net Pens	McCall Fish Hatchery	Omak Hatchery
Leaburg Hatchery	McKenzie	Oregon Hatchery Research Center
Leavenworth NFH	McKernan Hatchery	Oxbow (IDFG)
Lewis River Hatchery	Merced River Fish Hatchery	Oxbow (ODFW)
Lilliwaup Creek Hatchery	Merwin Fish Hatchery	Pahsimeroi
Little Port Walter Field Station	Methow Fish Hatchery	Parkdale Hatchery

Appendix C. Hatcheries (continued).

Pelton Ladder	SAFE Tongue Point Net Pens	Thornhollow Satellite
Pendleton Satellite	SAFE Youngs Bay Net Pens	Three Mile Dam
Pittsburg Landing Satellite	Salmon River Hatchery	Tonasket Pond
Powell Satellite	San Joaquin Fish Hatchery (SCRF)	Trask River Hatchery
Priest Rapids Fish Hatchery	Sandy River Hatchery	Trinity River Hatchery
Prosser Fish Hatchery	Sawtooth	Trojan Pond
Pullen Creek Hatchery	Sherars Falls Trap	Tucannon
Puyallup Hatchery	Silverado Fisheries Base	Tumwater Falls
Quilcene National Fish Hatchery	Similkameen Acclimation Pond	Turtle Rock Hatchery
Quinalt National Fish Hatchery	Skamania Hatchery	Twisp Rearing Pond
Rapid River	Sol Duc Hatchery	Umatilla Fish Hatchery
Red River Satellite	Soos Creek Hatchery	Upper Crooked River Satellite
Ringold Springs Hatchery	South Fork Salmon Satellite	Upper Grand Ronde Satellite
Riverside Pond	South Fork Walla Walla Hatchery	Voights Creek Hatchery
Roaring River Hatchery	South Santiam Hatchery	Wallace River
Robertson Creek Hatchery	Speelyai Fish Hatchery	Wallowa Fish Hatchery
Rock Creek Hatchery	Spring Creek NFH	Warm Springs Hatchery
Round Butte	Springfield Hatchery	Warm Springs NFH
Rowdy Creek Fish Hatchery	St. Marys Pond	Washougal Fish Hatchery
SAFE Blind Slough Net Pens	Sweetwater Springs	Wells Fish Hatchery

Appendix C. Hatcheries (continued).

Willamette Hatchery	Winthrop NFH	Yoosa-Camp Creek Satellite
Willard NFH	Wizard Falls Hatchery	



Appendix D. Valid Species List

Scientific Name	Common Name	Scientific Name	Common Name
<i>Acipenser transmontanus</i>	White Sturgeon	<i>Cottus leiopomus</i>	Wood River Sculpin
<i>Acrocheilus alutaceus</i>	Chiselmouth	<i>Cottus rhotheus</i>	Torrent Sculpin
<i>Alosa sapidissima</i>	American Shad	<i>Couesius plumbeus</i>	Lake Chub
<i>Ameiurus melas</i>	Black Bullhead	<i>Ctenopharyngodon idella</i>	Grass Carp
<i>Ameiurus nebulosus</i>	Brown Bullhead	<i>Cyprinus carpio</i>	Common Carp
<i>Carassius auratus</i>	Goldfish	<i>Esox lucius</i>	Northern Pike
<i>Catostomus ardens</i>	Utah Sucker	<i>Esox masquinongy x lucius</i>	Tiger Musky
<i>Catostomus catostomus</i>	Longnose Sucker	<i>Gambusia affinis</i>	Western Mosquitofish
<i>Catostomus columbianus</i>	Bridgelip Sucker	<i>Gila atraria</i>	Utah Chub
<i>Catostomus discobolus</i>	Bluehead Sucker	<i>Gila bicolor</i>	Tui Chub
<i>Catostomus macrocheilus</i>	Largescale Sucker	<i>Gila copei</i>	Leatherside Chub
<i>Catostomus platyrhynchus</i>	Mountain Sucker	<i>Ictalurus furcatus</i>	Blue Catfish
<i>Cichlasoma nigrofasciatum</i>	Convict Cichlid	<i>Ictalurus punctatus</i>	Channel Catfish
<i>Coregonus clupeaformis</i>	Lake Whitefish	<i>Lampetra tridentata</i>	Pacific Lamprey
<i>Cottus bairdi</i>	Mottled Sculpin	<i>Lepomis cyanellus</i>	Green Sunfish
<i>Cottus beldingi</i>	Piute Sculpin	<i>Lepomis gibbosus</i>	Pumpkinseed
<i>Cottus cognatus</i>	Slimy Sculpin	<i>Lepomis gulosus</i>	Warmouth
<i>Cottus confusus</i>	Shorthead Sculpin	<i>Lepomis macrochirus</i>	Bluegill
<i>Cottus extensus</i>	Bear Lake Sculpin	<i>Lota lota</i>	Burbot
<i>Cottus greeniei</i>	Shoshone Sculpin	<i>Micropterus dolomieu</i>	Smallmouth Bass

Appendix D. Valid Species List (continued).

Scientific Name	Common Name	Scientific Name	Common Name
<i>Micropterus salmoides</i>	Largemouth Bass	<i>Pimephales promelas</i>	Fathead Minnow
<i>Misgurnus anguillicaudatus</i>	Oriental Weatherfish	<i>Poecilia mexicana</i>	Shortfin Molly
<i>Mylocheilus caurinus</i>	Peamouth	<i>Poecilia reticulata</i>	Guppy
<i>Notropis hudsonius</i>	Spottail Shiner	<i>Pomoxis annularis</i>	White Crappie
<i>Noturus gyrinus</i>	Tadpole Madtom	<i>Pomoxis nigromaculatus</i>	Black Crappie
<i>Oncorhynchus clarkii</i>	Cutthroat Trout	<i>Prosopium abyssicola</i>	Bear Lake Whitefish
<i>Oncorhynchus clarkii bouvieri</i>	Yellowstone Cutthroat Trout	<i>Prosopium coulteri</i>	Pygmy Whitefish
<i>Oncorhynchus clarkii henshawi</i>	Lahontan Cutthroat Trout	<i>Prosopium gemmifer</i>	Bonneville Cisco
<i>Oncorhynchus clarkii lewisi</i>	Westslope Cutthroat Trout	<i>Prosopium spilonotus</i>	Bonneville Whitefish
<i>Oncorhynchus clarkii utah</i>	Bonneville Cutthroat Trout	<i>Prosopium williamsoni</i>	Mountain Whitefish
<i>Oncorhynchus kisutch</i>	Coho Salmon	<i>Ptychocheilus oregonensis</i>	Northern Pikeminnow
<i>Oncorhynchus mykiss</i>	Rainbow Trout/steelhead	<i>Pylodictis olivaris</i>	Flathead Catfish
<i>Oncorhynchus mykiss aguabonita</i>	Golden Trout	<i>Rhinichthys cataractae</i>	Longnose Dace
<i>Oncorhynchus mykiss gairdneri</i>	Inland Columbia Basin Redband Trout	<i>Rhinichthys falcatus</i>	Leopard Dace
<i>Oncorhynchus mykiss x clarkii</i>	Rainbow X Cutthroat Trout	<i>Rhinichthys osculus</i>	Speckled Dace
<i>Oncorhynchus nerka</i>	Sockeye Salmon or kokanee	<i>Richardsonius balteatus</i>	Redside Shiner
<i>Oncorhynchus tshawytscha</i>	Chinook Salmon	<i>Salmo salar</i>	Atlantic Salmon
<i>Osmerus mordax</i>	Rainbow Smelt	<i>Salmo trutta</i>	Brown Trout
<i>Perca flavescens</i>	Yellow Perch	<i>Salvelinus alpinus</i>	Arctic Char
<i>Percopsis transmontana</i>	Sand Roller	<i>Salvelinus alpinus oquassa</i>	Blue Backed Trout

Appendix D. Valid Species List (continued).

Scientific Name	Common Name	Scientific Name	Common Name
Salvelinus confluentus	Bull Trout	Salvelinus namaycush	Lake Trout
Salvelinus confluentus x fontinalis	Bull trout X brook trout	Salvelinus namaycush x fontinalis	Splake
Salvelinus fontinalis	Brook Trout	Stizostedion vitreum	Walleye
Salvelinus namaycush	Lake Trout	Thymallus arcticus	Arctic Grayling
Salvelinus namaycush x fontinalis	Splake	Tilapia aurea	Blue Tilapia
Stizostedion vitreum	Walleye	Tilapia mossambica	Mozambique Tilapia
Thymallus arcticus	Arctic Grayling		
Tilapia aurea	Blue Tilapia		
Tilapia mossambica	Mozambique Tilapia		
Tinca tinca	Tench		
Xiphophorus helleri	Green Swordtail		
F1 Hybrid	First Generation Hybrid		
F2 Hybrid	Second Generation Hybrid		
O. mykissBC	Backcross hybrid		
O. clarkiiBC	Backcross hybrid		
S. confluentusBC	Backcross hybrid		
S. fontinalisBC	Backcross hybrid		
Hyb	Hybrid		
Salvelinus confluentus	Bull Trout		
Salvelinus confluentus x fontinalis	Bull trout X brook trout		
Salvelinus fontinalis	Brook Trout		